

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 19, 2002, 13:36:37 : Search time 2342.25 Seconds
(without alignments)
5030.565 Million cell updates/sec

Title: US-09-788-476A-3
Perfect score: 873
Sequence: 1 tggagtgagggttaacaaga.....tgatattgtctgttaaat 873

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues
Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estbda:*
2: em_esthum:*
3: em_estlin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_estl:*
10: gb_est2:*
11: gb_hlc:*
12: gb_hlc:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrtl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	820	93.9	910	11	AF161434 Homo sapi
2	814.4	93.3	1070	10	BM460786 AGENCOURT
3	780	89.3	806	10	BG574651 60259653
4	759	86.9	783	10	BG910161 60280548
5	755	86.5	788	10	BM462456 AGENCOURT
6	749.4	85.8	783	10	BG533012 602580893
7	740.2	84.8	776	10	B1460375 602302043
8	738.2	84.6	887	10	B1255433 602977928
9	733	84.0	889	10	B1552670 603193915
10	725.4	83.1	774	10	B1870282 603393788
11	721	82.6	744	10	B1520421 603071604
12	713	81.7	744	10	BG493148 602541829
13	711.8	81.5	974	10	BG387900 602412920
14	710.6	81.4	781	10	BG720065 602691562
15	705.8	80.8	1139	10	BG289677 602384642
16	697.2	79.9	802	10	BG542056 602572169
17	663.8	76.0	1107	10	BG250284 602362415

18	662.4	75.9	699	10	BG261221 602372957
19	651.4	74.6	781	10	BG178461 602330263
20	651	74.6	685	10	BG390201 60245736
21	647	74.1	648	9	AV710050
22	640	73.3	799	10	BG500895 602547362
23	639.6	73.3	747	10	BE391455 601286447
24	635	72.7	718	10	BG502106 602548449
25	622.8	71.3	897	10	BF576251 602134108
26	616.6	70.6	798	10	BG323390 602421786
27	613.8	70.3	666	10	B1460158 603201744
28	612.4	70.1	683	10	BF092754 MR4-TN011
29	604	69.2	610	10	BG614223 602369906
30	598.6	68.6	1107	10	BF979954 602288518
31	595.2	68.2	754	10	BF663147 602139209
32	594.6	68.1	933	10	BG288241 602383764
33	592.8	67.9	893	11	AK003453 AK009455 Mus muscu
34	581.4	66.6	910	10	BE378791 601237288
35	576.2	66.0	699	10	B1961456 MON01_5_G
36	574.6	65.8	773	10	BE782311 601470086
37	571	65.4	571	10	BE887511 601508160
38	564.2	64.6	681	10	BE378430 601236768
39	558.4	64.0	577	9	AW131598 xcf11h09.x
40	557	63.8	784	10	BG254640 602368607
41	551.2	63.1	624	10	BF88562 MR4-TN011
42	551	63.1	562	9	BE018801 bb85b11.y
43	547	62.7	639	10	BE392774 601307843
44	544.8	62.4	631	10	BE390709 601286887
45	544	62.3	579	10	BG898224 HOA2-1-A-

ALIGNMENTS

RESULT	1	LOCUS	AF161434	DEFINITION	Homo sapiens HSPC316 mRNA, partial cds.	ACCESSION	AF161434	VERSION	AF161434.1	GI:6841281	KEYWORDS	human.	SOURCE	ORGANISM	REFERENCE	1 (bases 1 to 910)	AUTHORS	Fan,H.Y., Mao,Y.F., Dai,M., Huang,Q.H., Chen,S.J. and Chen,Z.	TITLE	Human partial CDS from cd34+ stem cells	JOURNAL	Unpublished	2 (bases 1 to 910)	FEATURES	source	1. 910	location/Qualifiers	1. 910	/organism="Homo sapiens"	/db_xref="taxon:9606"	/clone="CBIA1H07"	/cell_type="cd34+ stem cell"	/tissue_type="blood"	<1. 769	/codon_start=2	/product="HSPC316"	/protein_id="AA28994.1"	/db_xref="GI:6841282"	/translation="SGVGKMMATEVLEHLKLAIEKOCLEAGLETKGKODLIIR	LOALEEHAEEANEEDVLDGETTEETKPELTPVKEPEPEKVDVAARKVKYKITS	EIPTOTERMOKRAEPFNPVLESKKARARVIGSSVPNKRSVILITNMUTWLSLE	EUKDGLNVSISIKSDEDEKLRKRFRFGIVTSAGTGTEDEARRGEQSLGIP	DEKPLILSLQCPPELISFLVTYMPKCTVACLRAPO"
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RESULT	3
LOCUS	BG574651
DEFINITION	BG574651 806 bp mRNA linear EST 10-APR-2001
ACCESSION	602596653F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:4705620 5',
VERSION	BG574651
KEYWORDS	mRNA sequence.
SOURCE	BG574651.1 GI:13562304
ORGANISM	EST.
	human.
	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	1 (bases 1 to 806)
AUTHORS	NIH-MGC htcp://mgc.ncl.nih.gov/.
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-re@mail.nih.gov Tissue Procurement: DCTD/DPF CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov plate: LLM10572 row: 1 column: 13 High quality sequence stop: 806.
FEATURES	Location/Qualifiers
source	1. 806
	/organism="Homo sapiens"
	/db_xref="taxon:9606"
	/clone="IMAGE:4705620"
	/clone_lib="NIH_MGC_87"
	/tissue_type="mammary adenocarcinoma, cell line"
	/lab_host="DH10B (phage-resistant)"
	/note="Organ: breast; Vector: pCMV-SPORT6; Site: 1; NotI; Site: 2; SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.383 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."
BASE COUNT	263 a 155 c 211 g 177 t
ORIGIN	

Query Match	89.3%	Score 780:	DB 10:	Length 806:
Best Local Similarity	99.9%	Pred. NO. 3.7e-152:		
Matches 791:	Conservative 0:	Mismatches 0:	Indels 1:	Gaps 1:
QY 5	gtgaagggttaacaagatbtgcagaccagagaggttgcgtctccataaagctaaagcttgcgaa	64		
Db 15	GTGAGGGGTAAACAAGATGTGGCGACCGAGCGGTGGAGCTCCATAAGCTTAAGCTTGGCGAA	74		
OY 65	ctaaagcaagaatgtcttgcgtgtgtgttgcagaccaagggaataaagaatctatc	124		
Db 75	CTAAAGCAAGAATGCTCTTGTCTGTGGTTTGGAGACCAAGGGAATAAACAAGATCTTATTC	134		
OY 125	cacaaaccacagagctatcttgcagaacaatgtctgaagaaggagagcaaatgaagaagatba	184		
Db 135	CACAACTCCAGGCAATATCTTTGAAGAAATGCTGAAGAGGAGGCAAAATGAAGAGATGA	194		
OY 185	ctgggagatgaacaacagagaagaagaacaaagcccatctgagctctccctgcataaaggaa	244		
Db 195	CTGGGAGATGAAACAAGAGAGAAAGAAACAAAGCCCATTTGAGCTCCCTGCTCAAGAGGAA	254		
OY 245	gaacccctctgaaaaaactgtgtgaatgtgcagcagaagaagaatgtgtbaaataacatc	304		
Db 255	GAACCCCTCGAAAAAATCTGTGATGTGCACACAGGAAGAAAGTGCTAAAAATTAACAATCT	314		
OY 305	gaatcaccaagagctgcagagaatgcagaagaaggagctgaagcatcaatgtatcctgtgagc	364		
Db 315	GAATATCCACAGACTCGAAGAAATGCAGAAAGAGGCTGACCAATTCATATGTCCTGTGAGC	374		
OY 365	ttggaagatlaagaaagctgcgtcgcgcagctagttgttgcattcttcacgtccacaacaa	424		
Db 375	TTGAGAGTAAAGAAAGCTGCTCGGCGACGCTGAGTTGGGATTTCTTCAGTTCCAAACAAA	434		
OY 425	ggtctgtcatctgataaacaacctaigtttaactgcgtgaagcctgaaggaagaagctcaa	484		
Db 435	GGTCTGTATCTGATTAACAAACCTATGGTTTAACTTGGATTAAGCTGAAGGAAAGAGCTTCA	494		
OY 485	agatttgtttgaatgtctcttcaatcccaagaagcttgaagaatgtatgcagaacatgaa	544		
Db 495	AGATTGTGTTGAATGTCTCTTCAATCTCCAGAAAGTGTGAAGATGATGAGAAACTGAAA	554		
OY 545	aagagaagaagcgaattgcgattgtcacaagtlcagcttgcagtgaactbgaaccacagaagat	604		
Db 555	AAGAGGAAGGAGCGCAATTGGGATTTGTCCACAAGTTCAGCTGGAACCTGAACCAACAGAGAT	614		
OY 605	acagagggcaagaagaagaagaagaagcagaagcgttgcgttgcgtgttgaagaattcct	664		
Db 615	ACAGGGGCAAGAAAGAAAGGAAAAAGACCAAGCGCTTTGGGATTCCTGTATGAAAAATTCTCT	674		
OY 665	gatacttctgtctcgaagtgcttccaattctctcctctctctcttgcgtgcacataatgcc	724		
Db 675	GATACTTCTGTCTCCAGTGTCTTCCATTCTCCATTCTCTCTTCTTGAGTGCACATATATATGCC	734		
OY 725	taaatgcacagtcatagtgcctaagctgcctgcctcgc-aatgaaggagacatgtaaccagat	783		
Db 735	TAAATGCACAGCAATGTCTCTACGTCTGCGCTCGCAATATGAGGAGCATGTATACCCAGGT	794		
OY 784	acatcatgaac 795			
Db 795	ACATCATGAAAC 806			
RESULT 4				
LOCUS	BG910161	783 bp	mRNA	linear
DEFINITION	602805554861 NCL_CGAB_Brn67 Homo sapiens cdna clone IMAGE:4938082			
ACCESSION	BG910161			
VERSION	BG910161.1	GI:14290637		
KEYWORDS	EST.			
SOURCE	human.			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			


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Db      61 GATGTACTGGAGATGAAACAGAGAGAAAGAAACAAAGCCCATTTGATGCTCCCTGCAAA 120
QY      239 gaggaagaacccctgaaaaaacgtgtagtgcagagaagaagaagtgtgtaaat 298
Db      121 GAGGAAGAACCCCTGAAAAAACTGTGTATGTGGCAGCAGAAAGTGTGAAAT 180
QY      299 acactcgaataacacacagactgagaaatgcagaagaaggtctgaacgtatcaatctac 358
Db      181 ACATCTGAAATATCCACACACACTGAGAGATGACAGAAAGGCTGAACGATTCATCTACT 240
QY      359 gtgcagcttgagagtaagaagaagctgcgcgacgtgaagtttgagttcttcagttca 418
Db      241 GTGAGCTTGGAGAGTAAGAAAGCTGCTGGCAGCTAGGATTGGGATTCTTCAAGTTCCA 300
QY      419 acaaaaggtcgtatcctgcatacaaacctatggttaacttgatgaactgaagaaga 478
Db      301 ACAAAGGCTGTCATCTGATPACAAACCTATGGTTAACTTGAGTAAGCTGAAGGAAGA 360
QY      479 gctcaagaatttggttltgaatgctcttcaatctccagaagaagctgaagatgataaga 538
Db      361 GCTCAAGATTGGTGGTTGAATGTCCTTCATTCACAGAAAGTGTGAAGATGATGAGAAA 420
QY      539 ctgaaaaaagagaagagagcttggagattgacacagttcaagctggaactggaaccaca 598
Db      421 CTGAAAAAGAGGAAGAGACGATTTGGGATTTGCACAAAGTTCAAGCTGGAACACACA 480
QY      599 gagataacagggcaaaagaagaagaagaagacagccttgagattgctcgtatgaaga 658
Db      481 GAGGATPACAGAGGCAAAAGAGAGAAAGACAGAGCCCTTGGGATTGGCTGATGAAGAA 540
QY      659 gtctcgaacttcttctcctcagtggttccatcttccctcctccttctgtacata 718
Db      541 GTTCTGATCTTCTGTCTCCAGTGTTTCCATTCTCTCCTCTCTTGGTGCACATA 600
QY      719 tatgctaataatgcacagtcacatgctcctacgtccctgcctcgaatgaaggagatgacc 778
Db      601 TATGCTTAATATGCACAGTCATGTGCTACGTCCTGCGCAATGAGGAGCATGTACCC 660
QY      779 caggtacacatgaacagcggcagcagttgactatgctcgttccagcttaagtg 838
Db      661 CAGGATCATCATGAACGCGGACACAGTTGACTTATGCTGTTACGCTTTAAGGTTG 720
QY      839 ttgtgttttcttctgtatgattgtgtctgttaat 873
Db      721 TTGTGTTTTTGTGTTTGTATGTTGCTTGTAAAT 755

RESULT 6
BG533012 783 bp mRNA linear EST 03-APR-2001
LOCUS 602580893P1 NIH_MGC_61 Homo sapiens cDNA clone IMAGE:4718711 5',
DEFINITION mRNA sequence.
ACCESSION BG533012 GI:13524551
VERSION BG533012.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 783)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: CLONTECH Laboratories, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
http://image.lnl.gov
Plate: LNCM1570 row: j column: 24

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FEATURES
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        1..783
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone="IMAGE:4718711"
            /clone_1lb="NIH_MGC_61"
            /tissue_type="embryonal carcinoma"
            /lab_host="DH10B (T1 phage-resistant)"
            /note="Organ: testis; Vector: pDNR-LIB (Clontech); Site:1:
            SfiI (ggccgctcgcc); Site:2: SfiI (ggccatagcc);
            Double-stranded cDNA was prepared from cell line RNA. 5'
            and 3' adaptors were used in cloning as follows: 5'
            adaptor sequence: 5'-CAGGCGCATTTAGGCC-3' and 3' adaptor
            sequence: 5'-ATCTAGAGCCGACCGGCCGACATC-dfr(30)BN-3'
            (where B = A, C, or G and N = A, C, G, or T). Average
            insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies
            contained inserts by PCR. This library was enriched for
            full-length clones and was constructed by Clontech
            Laboratories (Palo Alto, Ca). Note: this is a NIH_MGC
            Library."

BASE COUNT 257 a 145 c 207 g 174 t
ORIGIN

Query Match 85.8%; Score 749.4; DB 10; Length 783;
Best Local Similarity 98.7%; Pred. No. 8.5e-146;
Matches 777; Conservative 0; Mismatches 6; Indels 4; Gaps 2;

QY      7 gagggtaacaagaatgagcagccgaacggtgagctccataagctaaagcttgcgaact 66
Db      1 GAGGGGTAAACAAGATGGGACCGAGCGGTGAGCTCATAGCTTAAGCTTGCCGAAT 60
QY      67 aaagcaagaatgcttctgctggttggagacaaaggaataaagcaagatcttatcca 126
Db      61 AAAGCAAGATGCTCTTGCTCGGTGGAGACCAAGGAATTAAGCAAGATCTTATCCA 120
QY      127 cagactccagagatattcttgaagaacatgcttaagaagaagaaatgaagaagatgact 186
Db      121 CAGACTCCAGGCTATATCTTGAAGAACTGCTAAGAGGCGCAATTAAGAAATGATGACT 180
QY      187 ggaagatgaacaagaagaagaacaagaaccatltgagctccctgtcaaaagaaga 246
Db      181 GGGAGATGAACAAGAGAAAGAAAGAAAGCCCAATGAGCTCCCTGCAAAAGAGAGA 240
QY      247 accccctgaaaaactgttgaatgtgtgcagcagaagaagaagtgtgaaataatcatcga 306
Db      241 GCCCCTGAAAAAAGCTGTGATGTGGCAGCAGAGAAAGTGTGAATTAATCAATCTGA 300
QY      307 aataccagagactgagagaatgcagaagaagggtcgaacgattcaatgtaactgtgagct 366
Db      301 AATACCAAGACTGAGAGATGCAAGAGAGGCTGACGATTCATTAATGACCTGTGAGCTT 360
QY      367 ggaagatgaagaagctgtcgcggcagctaggttlttggaatttctcaagttccacaaga 426
Db      361 GGAGAGTAAGAAAGCTGCGCGGACGCTAGGTTGGGATTTCTTCAGTTCCAAAGAAAG 420
QY      427 tctgtcatctgatacaaaaactatgttaactgtgataagctgaaggaagaagctcacaag 486
Db      421 TCTGTCACTGTGATPACAAACCTATGTTAACTTGATTAAGCTGAAGGAAGAGCTCAAG 480
QY      487 atttggttgaatgctcttcaatctccagaagaagctgaagaagttgtaagaacttgaaga 546
Db      481 ATTTGGTTGAATGTCTCTCAATCTCCGAAAGTCTGAAGATGATGAAGAACTGAAGAAA 540
QY      547 gaggaagagcgaatttgagattgtcaagaagttcaagctgaactggaacacacagagatcac 606
Db      541 GAGGAAGAGAGCATTTGGGATTTGCACAAAGTTCACTGGAATGGAACACAGAGAGATAC 600
QY      607 agagcgaagaagaagaagaagcagagcgttlttggaattcctcgaatgaagaagttcctga 666
Db      601 AGAGCAAAAGAGAGAGAAAGAGCAGAGAGCG-TTGAGGATTTGCTGATGAAGAAAGTCTCTGA 659

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Oy	667	tactctcgttcacgaagtcttccattctcctctcctctctcttgatgcacaatatagcca	726
Dd	660	TACTTTCCTTTCCAGGTGTTTTCCATTCTCCTCTCTTGCGACATATAAGCTTA	719
Oy	727	aatgcaaacatcatgtcgacctacgcctcctgcaaatgaggagcatgatccccaggtaca	786
Dd	720	AATGCACATCATGTGCCCTAAGCTGTGGCTGC---ATGAGGAGCATGTACCAGGATACA	776
Oy	787	tccatgta 793 	
Dd	777	TCCATGA 783	
RESULT	7		
LOCUS	B1460375	776 bp	mRNA linear EST 21-AUG-2001
DEFINITION	603202043r1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5267722 5'		
ACCESSION	B1460375		
VERSION	B1460375.1		
KEYWORDS	GI:15251031		
SOURCE	EST.		
ORGANISM	human. Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 776) NIH-MGC http://mgs.ccl.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC)		
JOURNAL	Unpublished (1999)		
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: Miklos Palkovits, M.D., Ph.D. cDNA Library Preparation: Michael J. Brownstein (NHGR), Shiroki Toshiyuki and Piero Carninci (RIKEN) cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov/ Plate: LLM11675 row: f column: 11 High quality sequence stop: 775. Location/Qualifiers 1..776 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:5267722" /clone.lib="NIH_MGC_97" /lab_host="DH10B" /note="Organ: testis; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gccgaae); Oligo-df primed using primer 5'-tttttttttttttvn-3'; size-selected for average insert size 2.2 kb and normalized to Rof 5. This is a primary library enriched for full-length clones and constructed using the cap-trapper method (Carninci, In preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health. Note: this is a NIH_MGC Library."		
FEATURES	source		
BASE COUNT	254 a	146 c	205 g
ORIGIN	171 t		
Query Match	Best Local Similarity	84.8%; Score 740.2; DB 10; Length 776;	
Matches	765; Conservative	0; Mismatches	3; Indels
Oy	7	gaggggttaaagaatgtagaccgaagaggtgagctcataaagctaagcttgcggaact	66
Dd	5	GAGGGGTAAACAAGAATGAGCACCGACGAGCGGTGAGCTCAATAGCTAAAGCTTGC GA ACT	64
Oy	67	aaagaagaatcttgtcgtcggtgtttgagaagcaaggaaataaagacaagatcttatca	126
Dd	65	AAAGCAAAGATGTCTTGCTCGTG GTTTGAGACCAAAGGAATPAAGAACAGATCTTATCCA	124

OY	127	cagactccaggatctcttgaagaacatgcgttaaaaggaggaaaattgaagaagtgtact	186
Dd	125	CAGACTCCAGGATATCTTGAAGAACAATGCTCTAAAGGGAGGCCAATAATGAAGAAGATGTACT	184
OY	187	ggagagatgaaacacagaggaaagaagaacaagcccaattgagctccccttgltcaaaagagaaaga	246
Dd	185	GGGAGATGAACACAGAGAAGAAAGAACCAAGCCCATTTGAGCTCCCTGTCTAAAGAGGAAGA	244
OY	247	accgccctgaanaaacctgtttgatgtgycagcagaagaagaagtgtgtgaataatcaatcttga	306
Dd	245	ACC GCC CTG AAAAA AC TGT GTT GAT GTG GC AG CAC AG A GA A AA GG CG TGA A AT TT ACA T TC GA	304
OY	307	aatacacacagacttggagagaatgcagaagaaggcttaacacctcaatlgaacctgttagactt	366
Dd	305	AAT ACC AC A G A C T G A G A G A N A T C A G A N A G G G C T G A C A C A T T C A A T G T R A C C T G T A G C T T	364
OY	367	ggagagtaagaagaagctgtcctcgggcagctaagtttggagatttccttcagtlccaacaagaag	426
Dd	365	GGAGAGTAAGAAGAAGCTGTCTCGGGCAGCTTAGTGTCGGGATTCTTCAGATTCCTCAACAAAAGG	424
OY	427	tctgtcatcttgttaacaacctaigtgttaacttggatgaatgcgaagagaagagctccaag	486
Dd	425	TCTGT CAT CTGTG TAACA AACCTTATGTTTACTTGGATTAGCTGAAGAGGAAGAGCTCAAAAG	484
OY	487	atttggtttgaatgtctctcttccaatccagaagaagctctgaaga tga tgaagaacttgaaaaa	546
Dd	485	ATT TG T T G A T T G A T G T C T C T T C A A T C T C C A G A A A G T C T G A A G A T G A T G A A A C T G A A A A A	544
OY	547	gagagaagaagcgaatttggatgtgtacaagaatgtcaagcttgcgaactggaaccaacagaagatc	606
Dd	545	GAGGAAGAGGCATTTGGATTTGGATTGTACAAAGTTCACACTGGAACTGGAAACCCAGAGAGATAC	604
OY	607	aagaagcaagaagaagaagaagaagcagagcgctcttggatcttgcctgaatgaagaagctctga	666
Dd	605	AGAGCAAAGAAGAGAGAAAGACAGAGAGCGCTTTGGAGATTGCTGATGAAAGTTCCCTGA	664
OY	667	taacttcgttctccagtggtttt-ccattctctccttcttcttcttggtcac--atatarg	723
Dd	665	TAC T T T C G T T T C C A G A G T T T T C C C A T T T C T C T C T T C T T G T G T C A C A T T A T A T G C	724
OY	724	cctaattgcacatcatctgtccactgctccgcctgcacatgaaggagagatgt	774
Dd	725	CTAAATGCACATCATGTGCTACGTCTCTGCCCGCCGCAATGAGGAGCATGT	775
RESULT	8		
B1255433		887 bp	mRNA linear EST 17-JUL-2001
LOCUS			
DEFINITION	602977928B1 NIH_MGC_12 Homo sapiens CDNA clone IMAGE:5122974 5',		
ACCESSION	B1255433		
VERSION	B1255433.1 GI:14808843		
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Euteria; Primates; Catarrhini; Hominiidae; Homo.		
TITLE	NIH-MGC http://mgc.nci.nih.gov/.		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Unpublished (1999) Contact: Robert Strusberg, Ph.D. Email: cgarbs-jremail.nih.gov Tissue Procurement: ATCC CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: Inyte Genomics, Inc. DNA Sequencing by: Inyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov plate: LHAM1300 row: g column: 07 High quality sequence stop: 801. Location/Qualifiers		

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			/clone_lib="NH_MGC_12"	
			/tissue_type="cervical carcinoma cell line"	
			/lab_host="DH10B"	
			/note="Organ: cervix; Vector: pCMV-Sport6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.4 kb. Library prepared by Life Technologies."	
BASE COUNT	299 a	160 c	231 g	197 t
ORIGIN				
Query Match	Best Local Similarity	84.6%;	Score 738.2;	DB 10; Length 887;
Matches 818;	Conservative 0;	Mismatches 3;	Indels 8;	Gaps 7.
Oy	9	ggggtacaagaatgagcgaccaggaacggtggaagtcctcaataagcttaagctccgaactaa	68	
Db	1	GGGGTAACAGATGCGCAGCCGAGCGGGTGAGCTTCATTAAAGCTTGGCGAAGCTTA	60	
Oy	69	agccaagtgtcttgctcgttgtttggaaggaccaagggaataaaggaagcttatcccaa	128	
Db	61	AGCAAGAATGTCTTCTCTGTGS-TTGAAGACCAGGAATTAAGCAAGATTTATCCACA	119	
Oy	129	gactccagcatatctttaagacacatgcttgaagaggaaggaagcaaatgaagaagatgtactg	188	
Db	120	GACTCCAGGCATATCTTGAGAACATGCTGAGAGAGGCAATATGAGAACATGTACTCG	179	
Oy	189	gagatgaaaacagaggaaagaacaagcccattgaagtcacctgcaagaagaaac	248	
Db	180	GAGATGAACAGAGAGACAGAGAACAAAGCCCATTGAGCTCCCTGTCAAAGAGGAAGAAC	239	
Oy	249	ccccgtaaaaaaccttbtatgtgagcagcagaagaagaagtgtgaatatcatctgaaa	308	
Db	240	CCCCGAAAAAAGCTTTGATGTGGCAGCAGAAAGAAAGTGGTGAATAATTACATCTGAAA	299	
Oy	309	taccacagactlgaagaatlgaagaagaggcttgaacgatltcaatgttacctgtgaagcttgg	368	
Db	300	TACCACAGACTGAGAGAAATGCGAAGAGGGCTGGAAGCATCATGTACTGTGAGACTTGG	359	
Oy	369	agagtaagaagaagctgcctcgagcagctaaggtttggatttctcagtlccacaanaagtc	428	
Db	360	AGAGTAAAGAAAGCTCTCGGCGAGCTAGG-TTGGGATTTCTTCAGTTCCAAACAAAAGTTC	418	
Oy	429	tgatctcgtataaacaactatggttaactttgataaagcttgaagaagaagcttcaagat	488	
Db	419	TGTCAATCGATTAACAACCTATGTTGTTAACTTGATTAAGCTGGAAGGAAGAGCTCAAAAGAT	478	
Oy	489	tttgtttgaatgtctcttcaatctccagaagaatcttgaagaatgtagaacgtgaanaaa	548	
Db	479	T--GGTGAATGTCTCTTCAATCTCCAGAAATCTGGAAGATGATGAGAACTGAAAAAAGA	536	
Oy	549	ggaaggaagcgaatttggatttgtcacaaagtlcagcttgaaccttgaaccacagaagatacag	608	
Db	537	GGAAGGAGCGA-TTGGGATTTGCACAAGTTGAGCTGGAACCTGAACCCACAGAGGATACAG	595	
Oy	609	aggcaaaagaaggggaagaagagcagagcgcttttggatttgcctgtatgaanaagttcctgata	668	
Db	596	AGGCAAAAGAGGAGAAAGAGCAGAGCGG-TTGGGATTTGCCGTGATGAAGAAAGTTCCGATA	654	
Oy	669	ctttctgtctcagtgatttccattctctctctctctctcttcttggatccatatgtccttaa	728	
Db	655	CTTTCTGTCTTCCAATGTTTTTCATTCTCTCTCTCTTTTGGTCAATATATGCTTAA	714	
Oy	729	tgcacagtcataitgtcctaagtcctgcctccgaataagaaggagatgtatcccaaggtacalc	788	
Db	715	TGCACAGTCATGTGCTTACGTCTG-CITGCAATGAGGAGCATGATGACCCAGGTATATC	773	
Oy	789	cataagctgcggcagcaggtttg-acttatgtctgtttcagctttaaagt	836	

RESULT	9
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LOCUS	B1552670
DEFINITION	603193915F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5265219 5',
ACCESSION	mRNA sequence.
VERSION	B1552670
KEYWORDS	B1552670.1 GI:15439982
SOURCE	EST.
ORGANISM	human.
REFERENCE	Homo sapiens
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
JOURNAL	1 (bases 1 to 889)
COMMENT	NIH-MGC http://mhc.nci.nih.gov/ .
	National Institutes of Health, Mammalian Gene Collection (MGC)
	Unpublished (1999)
	Contact: Robert Strausberg, Ph.D.
	Email: cgapbs-remail.nih.gov
	Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
	CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
	Toshiyuki and Piero Carninci (RIKEN)
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
	DNA sequencing by: Incyte Genomics, Inc.
	Clone distribution: MGC clone distribution information can be
	found through the I.M.A.G.E. Consortium/LNL at:
	http://image.lnl.gov
	Plate: L16M1668 row: n column: 04
	High quality sequence stop: 757.
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	/clone="IMAGE:5265219"
	/clone_1lb="NIH_MGC_95"
	/tissue_type="hippocampus"
	/lab_host="DH10B"
	/note="Organ: brain; Vector: pBluescript (modified
	pBluescript KS+); Site.1: BamHI; Site.2: SalI-XhoI (gtcagag
); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTNN-3',
	size-selected for average insert size 2.5 kb and
	normalized to ROP 5. This is a primary library enriched
	for full-length clones and constructed using the
	Cap-trapper method (Carninci, in preparation). Library
	constructed by M. Brownstein (NIH/NHGRI, National
	Institutes of Health). Note: this is a NIH-MGC Library."
BASE COUNT	295 a 162 c 232 g 200 t
ORIGIN	
Query Match	84.0%; Score 733; DB 10; Length 889;
Best Local Similarity	97.4%; Pred. No. 2.2e-142;
Matches 798: Conservative	0; Mismatches 15; Indels 6; Gaps 5;
7	gagggtaacaagaatgagcagcgaagcgttgagctcataaagcttgcgaact 66
5	GAGGGTAACAAGATGGCGACCGAGACCGGTGAGCTCATTAAGCTTAAAGCTTGGCGAACT 64
67	aaagcaagaatgtctgtcgttggttgtagacccaaggaaggaataaagcaagatctatcca 126
65	AAAGCAAGAATGTCTGTCGTCGTGGTAGACCAAGGAAATTAAGCAAGATCTTATCCA 124
127	cagactccaagcatatcttgaaagaacatgctggaagaaggcaaatgagaagaatgtact 186
125	CAGACTCCAGGCATATCTTTGAAGAACATGCTGAAGAAGGCAAAATGAAGAAGATGTACT 184
187	gggagatgaacaagaggaagaagaacaagcccatgagctccctgtccaagaggaaga 246
185	GGGAGATGAACAACAGAGGAAGAAGAACAAAGCCCATTTAGCTCCCTGTCAAGAGGAAGA 244
247	acccccctgaaaaaacatgttgatgtgtgcagcaggaagaagaatgtgtgaaataatcaatctga 306

FEATURES	LOCATION/Qualifiers
Db	245 ACCCCCTGAAAAACGTTGATGTGGACGACAGAAAGAAAGTGGTAAATTCATCTGA 304
Oy	307 aatccacagactgtgaggaatgcagaaagaggctaaagatccaatgtacctgtgaactt 366
Db	305 AATACACACAGACTGAGAGAAATGCAAGAGGGCTCAACGATTCATGTAACCTGACGTT 364
Oy	367 ggaagtaagaagaatgtctcggcgacgtatggtttggatcttcacgttcacaacaag 426
Db	365 GGAGAGTAAGAAAGCTGCTCGGGCAGCTAAGTTTGGGATTTCTTCACTTCCAAACAAAG 424
Oy	427 tctgtcatctgataaacaacctatggttaacttggataaagctgaagagagctcaag 486
Db	425 TCTGTCACTGTATACAAACCTATGTGTTAACTTGATTAAGTGAAGGAAGAGCTCAAG 484
Oy	487 attgtgttgaaatgtctcttcaatctccaagaagctgaagatgataagataaagaa 546
Db	485 ATTGTGTTGAATGTCCTCTTCAATCTCCAGAAAGTCTGAGATGATGAGAAACTGAAAAA 544
Oy	547 gaggaaaggacgatttggatgtgtacaaagtccaagctggaacttggaaacacagagatac 606
Db	545 GAGGAAGGAGCATTTGGGATGTGCAACAAGTTCAAGTGAAGTGAAGTGAAGGAGATAC 604
Oy	607 agagagcaagaagagagaaagacagagagcgcttggatgtcctgtatgaagatctcga 666
Db	605 AGAGGC -AAGAGAGAGAAAGAGAGAGAGCGCTTGGGATTTGGCTATGAAAGTTCTCTGA 663
Oy	667 taacttcgtctccagtgatttccatctctctctctctcttctgtgacatatgtccta 726
Db	664 TACTTCTGTGTTCTCCAGTG -TTTCCATTTCTCTCTCTTCTTGTGGTCAATATATGCCCT- 721
Oy	727 aatgcacagtcatagtgtcctacgtccctgcctcgcaatgaaggagc--atgtaccacagta 784
Db	722 AATGCACAGTCATGTGCTTACCTCTCTGCTCCCAATGAGGAGACCATATTACCCCGACTT 781
Oy	785 catccatgaactcgtgcagcagcagtttgactatctgtatct 823
Db	782 ACATCTTAACTGCGGAGACAG-TTGAAATTATGCTGTT 819
RESULT 10	
LOCUS	B1870282 774 bp mRNA linear EST 11-OCT-2001
DEFINITION	60539378881 NIH_MGC_90 Homo sapiens CDNA clone IMAGE:5403909 5',
ACCESSION	B1870282
VERSION	B1870282.1 GI:16043955
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE	NIH-MGC http://mgc.nci.nih.gov/ .
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT	Unpublished (1999) Contact: Robert Strusberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov Plate: LHAM12029 row: p column: 22 High quality sequence stop: 774.

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/tissue_type="adenocarcinoma, cell_line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: liver; Vector: pCMV-SPORT6; Site.1: NotI;
Site.2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by lile technologies.
Note: This is a NIH-MGC library."
BASE COUNT      254 a      145 c      201 g      173 t      1 others
ORIGIN

```

Query Match	83.1%	Score	725.4	DB	10	Length	774
Best Local Similarity	98.6%	Pred. No.	8.3e-141				
Matches	763	Conservative	7	Indels	4	Gaps	3

OY	11	ggaaacagatgaggacagagacggtgagagctccataaagctaaagtttccgaactaaag	70
Db	1	GGTAACCAAGATGGCGACCCGAGACGGGGAGCTCCATTAACCTAAAGCTTCCGAACCTAAAG	60
OY	71	caagaatgtcttcgcgtgagttcttgagaccaagggagataaagcaaatcttaaccaca	130
Db	61	CAGAATGTCCTTGGCTCGTGGTTTGGAGACCAAGGGAAATTAACCAAGATCTTATCCACACA	120
OY	131	ctccagacatctctgaagaacatgctgaagaaggagcaatgaaagaatgtaactgga	190
Db	121	CTCCAGGCATATCTTGAAGAACATCTGCTGAAGAGAGCCAAATGAAGAACATGTAAGGGA	180
OY	191	gattgaacacgagaagaagaagaacaaagcccatctgagctccctcgtaagaagaagacc	250
Db	181	GATGGAACCGAGGAAGAAACAAAGCCCATTAAGACTCCCTGTCAAGAGGAAGAACCC	240
OY	251	ccctgaaaaaacgtctgattgagtcgacgagaagaagaatggctgaataatcatctgaata	310
Db	241	CCTGAAAAAAGCTGTGATGTGGCAGCAGAGAAGAAAGTGTGAATAATTACATCTGAATA	300
OY	311	ccacagactgagagaatgacagaagaaggctgaacgaattcaatgtacctgctgagcttgag	370
Db	301	CCACAGACTGAGAGAAATGCAGAAAGGGCTGAACGATTAAGTAACTGTGAGCTTGAGGAG	360
OY	371	agtaagaagaagctgagctcgagcaagctagtttggagattcttcgttccaacaaaagcttc	430
Db	361	AGTAAGAAAGCTGCTCGGGCAGCTAGGTTGGATTCTTCAGTTCCACAAAGAGGTCTG	420
OY	431	tcatctgataacaaacctatggttaacttggataaagctaaagaaagctcaaatct	490
Db	421	TGATCTGATAACAAACCTATGGTTAACTTGGATTAACCTAAGGAAGAGCTCAAAATTT	480
OY	491	ggtttgaatgtctcttcaatctccagaaagcttgaagaatgatatgaagaacttgaaaaaag	550
Db	481	GGTTGAATGTCTCTTCATCTCCAGAAAGTCTGAAGATGATGAGAACATGAAAAAGAGG	540
OY	551	aagagcgcatctgggagattgttcacaagttcaagcttgaagctggaaaccaagaagataaag	610
Db	541	AAGGAGCGCTTTGGGATTTGTCACAGTTTACAGTGAACGTGAACCCACAAAGGATTAAGAG	600
OY	611	gcaagaagaagaaagaagcagagcgcttggagattgagctgataa--aagttccgtatag	669
Db	601	GCAAGAAGAGGAAAAAGACACAGCGCTTTGGGATTGCTCGATGAACAAGTTCTCTATAC	660
OY	670	ttcttcg--ttctccagtglttccatattctctctctctc--ttgttcacatatatgcta	726
Db	661	TTTCTGTTCTCCACATGTTGTTTCATATTTCTCTCTCTCTTGTGGCACATATATATCTTA	720
OY	721	aatgacagatcatgtgctcagatgctctgctcgtcagatgaagagagcatatgtaacca	780
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/clone="IMAGE:5403909"	
/clone_id="NIH_MGC_90"	

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DEFINITION	
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BI52071604F1 NIH_MGC_119	linear EST 29-AUG-2000
Homo sapiens CDNA clone IMAGE:5163673 5',	
mRNA sequence.	

ACCESSION B1520421
 VERSION B1520421.1 GI:15345213
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 817)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
 Plate: LLM1406 row: 9 column: 02
 High quality sequence stop: 809.
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 /db_xref="taxon:9606"
 /clone_1b="IMAGE:5163673"
 /clone_1lb="NIH_MGC_119"
 /tissue_type="medulla"
 /lab_host="DH10B"
 /note="Organ: brain; Vector: pCMV-Sport6; Site_1: NotI;
 Site_2: EcoRV (destroyed); RNA source normal medulla from
 anonymous male age 27. Library is oligo-dT primed and
 directionally cloned (EcoRV site is destroyed upon
 cloning). Average insert size 1.3 kb, insert size range
 0.9-3 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (Invitrogen). Research Genetics tracking code 013. Note:
 this is a NIH MGC library."
 BASE COUNT 256 a 154 c 227 g 180 t
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 Best Local Similarity 97.7%; Pred. No. 6.8e-140;
 Matches 763; Conservative 0; Mismatches 15; Indels 3; Gaps 3;
 QY 1 tgaagtgaagggttaacaagatgacgacgagcggtgagctcacaatgaagctgtgc 60
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 DB 37 TCGAGTGAAGGGTAAACAAGATGCGACCGAGACGCTGAGCTCATAGCTAAAGCTTGC 96
 QY 61 cgaactaaagaagaatgctgt 120
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 DB 97 CGAAGTAAAGCAAGAAATGCTGCTCGTGGTGTGAGACCAAGGCAATAAAGCAAGATCT 156
 QY 121 tatccacagactccagcagcatcttgaagaacatgctgaagaaggaggaatgaagaaga 180
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 DB 157 TATCCACAGACTCCAGCATTTCTTGAAGAATGCTGAAGAGGCGCAATTAAGAAGA 216
 QY 181 tctactggtgagatgaacacagaggaagaagaacaaagcccatgtagctccctgtcaaga 240
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 DB 217 TGTAAGTGGAGATGAACAGAGCAAGAAAGAAAGCCCATGTGAGCTCCCTGTCAAGA 276
 QY 241 ggaagaacccccctgaaaaaaactgt 300
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 DB 277 GGAAGAACCCCTTAAATACTGTGTGATGTGTGACAGAGAAAGAAAGGTGAATAATTAC 336
 QY 301 atctgaataccacagactgagagatgcagaagaagggtcaaacgattcaatgtacctgt 360
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 DB 337 ATCTGAATATCCACAGACTGAGAGATGCAAGAGGCGCTAAGCATTTGATCACTGT 396
 QY 361 gagcttggagagtaagaagagctgtctgggacagctaggtttgggaattcttcagttccaac 420
 |||||||

DB 397 GAGCTTGAGAGTAAGAAAGCTGCTCGGCGACGTAGGTTTGGATTCTTCAGTTCCAAC 456
 QY 421 aaaagctgtcatctgataaacaacctatgttaaccttgataagctgaagaagagc 480
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 DB 457 AAAGGCTGTGATCTGTATACAAACCTATGTTAACTTGATAGCTGAAGAGAAAGAGC 516
 QY 481 tcaagaatttgattgtaattgtctctcaatctccagaagaagctgaagaatgaagaact 540
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 DB 517 TCAAGATGTCGTTTGAATGCTCTTCAATCTCAGAAAGCTGAGATGATGAAGAACT 576
 QY 541 gaaaagaaggaagagcagatttggatgtgtcaagttcagctgagactggaaccacaga 600
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 DB 577 GAAAAGGAGGAGAGGAGGATTTGGGATTTGTCACAAAGTTACCTGAACTGAAACACAGA 636
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 DB 637 GGATACAGAGGCAAGAGAGAGAAAGAGCAGACGCTTGTGGATTGGCTCGAAGAAAG 696
 QY 660 ttctgtactcttctgtctcagtgatttccattctctctctctctctgtgtaca-ta 718
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 DB 697 TTCTGATACCTTCTGTTCTTCACAGTGTTCATTTCTCTCTCTCTCTGTCACATTA 756
 QY 719 tatgtctaataatgcacagtcacatgtgc-taagctctgctcgcgaatgaggaagatgacc 777
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 DB 757 TATGCTTAATTTGCCAGTATGTGCTTACGCTCTGCTCGCATGAGGAGACATGTATAC 816
 QY 778 c 778
 DB 817 c 817
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 DEFINITION 602541829F1 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:4672974 5',
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 ACCESSION BG493148
 VERSION BG493148.1 GI:13454660
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 744)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
 Plate: LLM1490 row: 1 column: 07
 High quality sequence stop: 731.
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 /clone_1b="IMAGE:4672974"
 /clone_1lb="NIH_MGC_59"
 /tissue_type="mucoepidermoid carcinoma"
 /lab_host="DH10B (T1 phage-resistant)"
 /note="Organ: lung; Vector: pBMR-LIB (Clontech); Site_1:
 SfiI (99ccgctcgagc); Site_2: SfiI (99ccatcatgagc);
 Double-stranded cDNA was prepared from cell line RNA. 5'
 and 3' adaptors were used in cloning as follows: 5'
 adaptor sequence: 5'-CACGGCCATTAAGGCC-3' and 3' adaptor
 sequence: 5'-ATTCTAGAGCGCCAGGCGCCGACATG-dT(30)BN-3'
 (where B = A, C, or G and N = A, C, G, or T). Average

Insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, Ca). Note: this is a NIH_MGC Library "

BASE COUNT 248 a 131 c 200 g 164 t 1 others
ORIGIN

Query Match 81.7%; Score 713; DB 10; Length 744;
Best Local Similarity 98.4%; Pred. No. 3,1e-138;
Matches 730; Conservative 0; Mismatches 11; Indels 1; Gaps 1;

OY 1 tggagtgagggttaacaagatgagcagcggttgaggtccataagcttaagcttgc 60
DB 4 TGGAGTGGAGGGGTACCAAGATGCGACCGAGCGGTGGAGCTCCATTAAGCTTAAGCTTGC 63
OY 61 cgaactaaagcaagaatgtcttcgtcgtgtgttggaagcaaggaataaagaagatct 120
DB 64 CGAACTAAAGCAAGATGTCTGCTGCTGGTTGAGACCAAGGGAATTAACCAAGATCT 123
OY 121 tatccacagactccaggcatctctgaaagaactgctgaagaggaggaacaatgaaaga 180
DB 124 TATCCACAGACTCCAGGCTATCTTGAAGACATGCTGAAGGAGGCAATGAAGAGA 183
OY 181 tgtactggagatgaacacagaggaagaaacaaagccattgagcttccctgtcaaga 240
DB 184 TGTACTGGAGATGAACAGAGAGAAGAAACAAAGCCCATTTGAGCTCCCTGCAAGA 243
OY 241 ggaagaacccccgtgaaaaaactgttgatgtgcagcagagaagaagaatggtgaaat 300
DB 244 GGAAAGACCCCTGAAAAAACTGTGATGTGGCAGCAGAGAAAGTGTGAAAAATTAC 303
OY 301 atctgaatatccacagactgagagaatgcagagaagggtcgaagcatcaatgatact 360
DB 304 ATCTGAATACCAAGACTGAGAGAAATGCAGAGAGGCTGAACATTAATGTAATCT 363
OY 361 gagcttgagagtaagaagctgtctcgggcagctaggttggtgattcttcagttccaa 420
DB 364 GAGCTTGGAGATGAAGAAAGCTGCGGCGACCTAGTTGGATTTTCAGTTCCAAAC 423
OY 421 aaaaagctgtcatctgtaacaacataatggttaacttggttaagctgaaagaagaagc 480
DB 424 AAAAGTCTGTATCTGATTAACAACCTATGTTAACTTGATGATGAAGAGAAAGAC 483
OY 481 tcaaaagatttggttgaatgctctcctcaatcccaagaagctgaagatgaaagaact 540
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OY 541 gaaaaagaggaagagcgaatttggatgtgcacaagtccaagctgaagctgaaacacaga 600
DB 544 GAAAAAGAGGAAGGAGCGA-TTGGGATTTGTCACAAGTTCAAGCTGGAACGGAACACAGA 602
OY 601 ggaatcaagaggaagaagaggaagaagagcagcttgatgctgctgtgtaagaagt 660
DB 603 GGATTCAGAGGGAAAGAAAGAGGAAAGAGCAGAGCGCTTGGGANTGCTTGTAAGAAAT 662
OY 661 tccatgaacttctgtctcagatgtttccatctctctcctctcttctgtgcacatata 720
DB 663 TCCATATACTTCTGTGCTCCAGGTGTTTCCATTTCTCTCTCTCTCTGCGTCACATATA 722
OY 721 tgcctaaatgcacagcatgtg 742
DB 723 TGCCTAATGCACAGTCATGTG 744

RESULT 13
LOCUS BG387900 974 bp mRNA linear EST 12-MAR-2001
DEFINITION 602412920F1 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:4521268 5',
ACCESSION BG387900
VERSION BG387900.1 GI:13281346

KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE NIH-MGC <http://mgc.ncl.nih.gov/>.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLES Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgaab@remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LMNL at: <http://image.llnl.gov>
Plate: LLM10420 row: h column: 05
High quality sequence stop: 759.

FEATURES

source

1..974

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:4521268"

/tissue_type="embryonal carcinoma, cell line"

/lab_host="DH10B (phage-resistant)"

/note="Organ: testis; Vector: pCMV-Sport6; Site.1: NCI; Site.2: Sall; Cloned unidirectionally; oligo-dT primed. Average insert size 2.5 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."

BASE COUNT 326 a 218 c 245 g 185 t
ORIGIN

Query Match 81.5%; Score 711.8; DB 10; Length 974;
Best Local Similarity 98.1%; Pred. No. 5.5e-138;
Matches 741; Conservative 0; Mismatches 12; Indels 2; Gaps 2;

OY 14 aacaagatgagcgaacccgagagcgttgagctccataagcttaagcttgcgaactaaagcaa 73
DB 1 AACCAAGATGCGCACGAGCGGTGAGCTCCATTAAGCTTAAGCTTCCGAACTTAAGCAA 60
OY 74 gaatgctgttcgcgtgtgttggaagcaaggaataaagaagatcttaaccagactc 133
DB 61 GATGCTTGTGCTGCTGCTTGTGAGACCAAGGAAATTAACCAAGATCTTCCACAGACT 120
OY 134 cagcatalcttgaagaacatgctgaagaagaggaacaaatgaagaatgatactggagat 193
DB 121 CAGCATATCTTGAAGAACATCTGTAAGAGAGCAAAATGAAGAGATGTAAGTGGAGAT 180
OY 194 gaaacagaggaagaagaacaaagcccatgtgctccctgttaagaaggagaagaccct 253
DB 181 GAACAGAGAGGAAGAAACAAAGCCCATTTGAGCTCCCTGTTAAAGAGGAAGACCCCT 240
OY 254 gaaaaaacgttgatgtgcagcagagaagaagaatggtgtaaaatctatactctaaataca 313
DB 241 GAAAAAAGCTTGATGTGCGACAGAGAAAGAGTGTAAATTAATCAATCTAAATACCA 300
OY 314 cagactgagaagaatgcagaagaaggctgaacgatccaatgatactgctgtgagcttgaga 373
DB 301 CAGACTGAGAGAAATGCAGAGAGGCGTGAACGATTAATGTAATGTAAGTGGAGAGT 360
OY 374 aagaagctgtcgcggcagctaggttggatcttcctcagttccaaacaaagctgtgca 433
DB 361 AAGAAAGCTGCTCGGCGACCTAGGTTGGATTTCTTCAAGTTCCAAACAAAGCTGTGCA 420
OY 434 tctgataaacaacctatgcttaactgtgaagctgaaaggaagaagctcaagaatgtgt 493
DB 421 TCTGATTAACAACTATGTTACTTGGATTAAGCTGAAGGAAGAGCTCAAGATTTGGT 480

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLM10400 row: d column: 12
 High quality sequence stop: 697.

FEATURES

source

Location/Qualifiers
 1. 1139
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_image="4513499"
 /clone_lib="NIH_MGC_93"
 /issue_type="transitional cell papilloma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: bladder; Vector: pCW-SPOB6; Site: 1; NotI;
 Site: 2; SalI; Cloned unidirectionally; oligo-dr primed.
 Average insert size 1.7 kb. Library enriched for
 full-length clones and constructed by Life Technologies.
 Note: this is a NIH_MGC Library."

BASE COUNT 380 a 224 c 315 g 219 t 1 others
 ORIGIN

Query Match 80.8%; Score 705.8; DB 10; Length 1139;
 Best Local Similarity 94.7%; Pred. No. 9,6e-137;
 Matches 785; Conservative 0; Mismatches 37; Indels 7; Gaps 5;

OY 9 ggggtaacaaagatgagccgagagcgtgagatcctaagtaagcttcggaactaa 68
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 1 GGGGTAAACAAGATGGCGACGAGACGGTGGAGCTCCATTAAGCTTAAGCTTGGCAACTAA 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 OY 69 agcaagaatgctctgctcgctgcttggagagcaaggaagaaataagcaagatctatccaca 128
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 61 AGCAAGAAATGCTTCTGCTGCTGTTGGAGACCAAGGAAATAAGCAGATCTTATCCACA 120
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 OY 129 gactccaggcatatcttgaagaacatgctgaagagaggaagcaaaatgaagaagatgactgg 188
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 121 GACTCCAGGCAATATCTTGAAGAACATGCTGAAGAGAGGCAATGAAGATGTAATCTGG 180
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 OY 169 gagatgaacaaagagaaagaaagaaagccatctgagctccctgtcaagaggaagaac 248
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 DB 181 GAGATGAACAGAGAGAGAAACAAAGCCATTGAGCTCCCTGTCAAAAGAGAGAAAC 240
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 OY 249 cccctgaaacaaactgtgagctgagcagcagaaagaaatggatgaatctacatctgaaa 308
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 DB 241 CCCCTGAACAACTGTTGATGTGGCAGCAGAGAAAGTGTGAATAATTACATCTGAAA 300
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 OY 309 taacacagaactgagaagaatgcaagaagggctgaacgaltcaatgactgtgagcttgg 368
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 DB 301 TACCACAGACTGAGAGAAATGAGAAAGGGCTGAACGATTCAATGTAATCTGTGAGCTTGG 360
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 OY 369 aagatgaagaagactgctcgggagctaggttggagattcttcagttccacaagaagctc 428
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 DB 361 AGAGTAAGAAAGCTGCTCGGCGAGCTAGGTTGGGATTTCTTCAGTTCCAAACAAAGGTC 420
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 OY 429 tgtcatctgataaacaacctatggttaacttgataagctgaaggaagaaagctcaaaagt 488
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 DB 421 TGTCAATCTGATTAACAACCTATGTTAACTTGATTAAGCTGAAGGAAGAGCTCAAGAT 480
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 OY 489 ttggtttgaaatgtctcttcaatctccagaagatctgaagaatgaatgaagaatctgaaga 548
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 DB 481 TTGGTTTGAAATGTCTTCAATCTCCAGAAAGTCTGAAGATGATGAGAAACTGAAAAAGA 540
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 OY 549 ggaaggaagcatttggatgtgcacaagtctgagctggaacttggaaccacagaggtatcag 608
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 DB 541 GGAAGAGAGGATTTGGAGTTGTACAAAGTTCAAGCTGGAACCTGAACCAACAGAGATACAG 600
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 OY 609 aggcacaagaagaagaagaagcagagcgttggagatgcccgaatgaagaatcttcgata 668
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 601 AGGCAAGAAGAGAGAAAGAGCAGACGCTT--GGGATTTGCTGATGAAAAAGTT-CTGATA 657
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 OY 669 cttctgtctccagtgcttccatctctcc-ctctctgtgtacacatataatgcctaa 727
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 658 CTTTCGTTCTCCAGAGTGTTCATTTCTCTTCTTGGTGACATATATTGCTTA 717
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 OY 728 atgcacagcatgctcctacgctccgctcgcgaatga-9gagagcatgtacccca--ggta 784
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 718 AATGCCAGTCATGTGCTACGTCTGGCTGCGCAATGAGGGGAGCATGTTCCCATGCTAC 777
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 OY 785 catcatgaactgcgacgaagcttgaactatgtctgttcagctttaa 833
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 778 ACTCCCTTGACTGCGGCGCGCTTTGCTAAATTTGCGGCTTCAACGCTTA 826
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